

Filename : Phrixothrix vivianii lateral lanterns green light-eliciting
 luciferase cDNA and deduced primary structure.
 Sequence Size : 1746
 Sequence Position: -25 - 1746

Translation Position: 1 - 1635;

Genetic Code : Universal (amino-acid residues are in 3 letter code)

-20 -10
 TCAAGTCAAGACTTTAGGG

10 20 30 40 50
 ATCAAAATGGAAGAGAAACATTAGGCATGGAGAGCGTCCTCGTGATATAGTCCATCCT
 MetGluGluGluAsnIleArgHisGlyGluArgProArgAspIleValHisPro

60 70 80 90 100 110
 GGCTCGGCAGGACAACAATTATACCAATCATTTGTATAAATTTGCATCTTTTCTGTAAGCA
 GlySerAlaGlyGlnGlnLeuTyrGlnSerLeuTyrLysPheAlaSerPheProGluAla

120 130 140 150 160 170
 ATAATCGATGCTCATACAAATGAAGTAATATCATATGCTCAAAATATTTGAAACCAGCTGC
 IleIleAspAlaHisThrAsnGluValIleSerTyrAlaGlnIlePheGluThrSerCys

180 190 200 210 220 230
 CGCTTAGCTGTAGTATAGAACAATATGGCTTGAATGAAACAATGTTGTGGGTGTATGC
 ArgLeuAlaValSerIleGluGlnTyrGlyLeuAsnGluAsnAsnValValGlyValCys

240 250 260 270 280 290
 AGTGAAACAAATATAAACTTTTTTAAACCTGTCTTGCTGCTTTTATACCTTAGGAATACCA
 SerGluAsnAsnIleAsnPhePheAsnProValLeuAlaAlaLeuTyrLeuGlyIlePro

300 310 320 330 340 350
 GTAGCAACATCAAATGATATGTACACAGATGGAGAGTTAACTGGTCATTTGAATATATCA
 ValAlaThrSerAsnAspMetTyrThrAspGlyGluLeuThrGlyHisLeuAsnIleSer

360 370 380 390 400 410
 APACCAACTATCATGTTTGTAGTTCAAAGAAAGCACTCCCGCTTATTCTGAGAGTACAGCAA
 LysProThrIleMetPheSerSerLysLysAlaLeuProLeuIleLeuArgValGlnGln

420 430 440 450 460 470
 AATCTAAGTTTTCATTAAAAAAGTCGTAGTTATCGATAGCATGTACGACATTAAATGGCGTT
 AsnLeuSerPheIleLysLysValValValIleAspSerMetTyrAspIleAsnGlyVal

480 490 500 510 520 530
 GAATGCGTATCTACCTTTGTGTCACGTTAFACTGACCCACACCTTTGATCCATTGTCAATTT
 GluCysValSerThrPheValAlaArgTyrThrAspHisThrPheAspProLeuSerPhe

540 550 560 570 580 590
 ACACCAAAGATTTTGATCCCCTTGAAAAAATCGCATTAAATTATGTCATCATCTGGAACA
 ThrProLysAspPheAspProLeuGluLysIleAlaLeuIleMetSerSerSerGlyThr

FIG. 1A

600 610 620 630 640 650
ACTGGATTGCCTAAGGGTGTAGTACTGAGCCATAGAAGTCTAACTATAAGATTTCGTTTCAT
ThrGlyLeuProLysGlyValValLeuSerHisArgSerLeuThrIleArgPheValHis

660 670 680 690 700 710
AGCAGGGATCCCATTTATGGCACTCGTACGGTTCCACAAACATCAATTCTTTCTTTAGTA
SerArgAspProIleTyrGlyThrArgThrValProGlnThrSerIleLeuSerLeuVal

720 730 740 750 760 770
CCGTTCATCATGCCTTTGGAATGTTTACTACATTATCTTACTTTGTAGTAGGACTTAAG
ProPheHisHisAlaPheGlyMetPheThrThrLeuSerTyrPheValValGlyLeuLys

780 790 800 810 820 830
GTTGTAATGTTGAAGAAATTTGAGGGCGCACTTTTCTTAAAAACCATACAGAATTACAAA
ValValMetLeuLysLysPheGluGlyAlaLeuPheLeuLysThrIleGlnAsnTyrLys

840 850 860 870 880 890
ATCCCCACTATTGTAGTGGCCCCCTCCAGTTATGGTGTTTTTGGCTAAAAGCCCCATTAGTC
IleProThrIleValValAlaProProValMetValPheLeuAlaLysSerProLeuVal

900 910 920 930 940 950
GATCAATACGATTTATCGAGCTTAACGGGAAGTTGCTACTGGAGGAGCTCCTTTAGGAAAA
AspGlnTyrAspLeuSerSerLeuThrGluValAlaThrGlyGlyAlaProLeuGlyLys

960 970 980 990 1000 1010
GATGTCGCAGAAAGCAGTAGCAGAGAGGTTGAAATTACCTGGAATCATACAAAGGATATGGA
AspValAlaGluAlaValAlaLysArgLeuLysLeuProGlyIleIleGlnGlyTyrGly

1020 1030 1040 1050 1060 1070
TTAACTGAAACTTGCTGCGCTGTAATGATTACCCCTCATATGCTGTGAAACAGGTTCA
LeuThrGluThrCysCysAlaValMetIleThrProHisAsnAlaValLysThrGlySer

1080 1090 1100 1110 1120 1130
ACTGGAAGACCCCTTGCCATACATTAPAGCTAAAGTTTTAGATAACGCTACTGGGAAGGCG
ThrGlyArgProLeuProTyrIleLysAlaLysValLeuAspAsnAlaThrGlyLysAla

1140 1150 1160 1170 1180 1190
CTAGGACCAGGAGAAAGAGGCGAATATGCTTTCAAAGTGAAATGATTATGAAAGGATAT
LeuGlyProGlyGluArgGlyGluIleCysPheGlnSerGluMetIleMetLysGlyTyr

1200 1210 1220 1230 1240 1250
TACAACAAATCCGGAAGCAACTATTGATACTATTGACAAAGATGGTTGGCTTCATTCTGGA
TyrAsnAsnProGluAlaThrIleAspThrIleAspLysAspGlyTrpLeuHisSerGly

1260 1270 1280 1290 1300 1310
GATATTGGATATTACGACGAAGATGGAAATTTCTTTATAGTTGATCGATTGAAAGAACTT
AspIleGlyTyrTyrAspGluAspGlyAsnPhePheIleValAspArgLeuLysGluLeu

1320 1330 1340 1350 1360 1370
ATTAAATACAAGGGATATCAGGTTGCGCCTGCTGAACTGGAATCTGCTTTTACAACAT
IleLysTyrLysGlyTyrGlnValAlaProAlaGluLeuGluAsnLeuLeuLeuGlnHis

1380 1390 1400 1410 1420 1430
CCAAGTATTGCTGATGCGGGTGTACTGGAGTTCCGGACGAATTTGGTGGACAATTACCT
ProSerIleAlaAspAlaGlyValThrGlyValProAspGluPheGlyGlyGlnLeuPro

FIG. 1B

FIG. 1C

Filename : PhREcDNA
Sequence Size : 1720
Sequence Position: -40 - 1760
Translation Position: 1 - 1638;
Genetic Code : Universal (amino-acid residues in 1 letter code)

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                -30      -20      -10
          GTGACAGTTTAGTTTCAGTAGAAGATTTTTTTTGAGATCAAA

      10      20      30      40      50      60
ATGGAAGAAGAAAACGTTGTGAATGGAGATCGTCCTCGTGATCTAGTTTTTCCTGGCACA
M E E E N V V N G D R P R D L V F P G T

      70      80      90     100     110     120
GCAGGACTACAATTATATCAATCATTATATAAATATTCATATATTACTGACGGAATAATC
A G L Q L Y Q S L Y K Y S Y I T D G I I

     130     140     150     160     170     180
GATGCCCATACCAATGAAGTAATATCATATGCTCAATATTTGAAACCGCTGCCGCTTG
D A H T N E V I S Y A Q I F E T S C R L

     190     200     210     220     230     240
GCAGTTAGTCTAGAAAAATATGGCTTGGATCATAACAAATGTTGTGGCAATATGCAGTGAA
A V S L E K Y G L D H N N V V A I C S E

     250     260     270     280     290     300
AACACATACACTTTTTTGGCCCTTTAATTGCTGCTTTATACCAAGGAATACCAATGGCA
N N I H F F G P L I A A L Y Q G I P M A

     310     320     330     340     350     360
ACATCAATGATATGTACACAGAAAGGGAGATGATTGGCCATTTGAATATATCGAAACCA
T S N D M Y T E R E M I G H L N I S K P

     370     380     390     400     410     420
TGCCTTATGTTTTGTTCAAAGAAATCACTCCCATTATTCTGAAAGTACAAAAACATCTA
C L M F C S K K S L P F I L K V Q K H L

     430     440     450     460     470     480
GATTTCCCTTAAAGAGTCATAGTCATTGATAGTATGTACGATATCAATGGCGTTGAATGC
D F L K R V I V I D S M Y D I N G V E C

     490     500     510     520     530     540
GTATTTAGCTTTGATTACGTAATCTGATCAGCCTTTGATCCAGTGAAATTTAACCCA
V F S F D S R N T D H A F D P V K F N P

     550     560     570     580     590     600
AAAGAGTTTGATCCCTTGGAAGAAGACCGCATTAATTATGACATCATCTGGAACAACCTGGA
K E F D P L E R T A L I M T S S G T T G

     610     620     630     640     650     660
TTGCCTAAAGGGGTAGTAATAAGCCATAGAAGTATAACTATAAGATTCTGTCATAGCAGT
L P K G V V I S H R S I T I R F V H S S
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FIG. 2A

670 680 690 700 710 720
GATCCCATCTATGGTACTCGTATTGCTCCAGATACATCAATTCTTGCTATAGCACCGTTC
D P I Y G T R I A P D T S I L A I A P F

730 740 750 760 770 780
CATCATGCCTTTGGACTGTTTACTGCACTAGCTTACTTTCCAGTAGGACTTAAGATTGTA
H H A F G L F T A L A Y F P V G L K I V

790 800 810 820 830 840
ATGGTGAAGAAATTTGAGGGCGAATTCTTCTTAAACCATAACAAATACAAATCGCT
M V K K F E G E F F L K T I Q N Y K I A

850 860 870 880 890 900
TCTATTGTAGTTCCTCCTCCAATTATGGTATATTTGGCTAAAAGTCCATTAGTCGATGAA
S I V V P P P I M V Y L A K S P L V D E

910 920 930 940 950 960
TACAATTGCTCGAGCTTAACGGAAATTGCTAGTGGAGGCTCTCCTTTAGGAAGAGATATC
Y N C S S L T E I A S G G S P L G R D I

970 980 990 1000 1010 1020
GCAGATAAAGTAGCAAGAGATTGAAAGTACATGGAATCCTACAAGGATATGGATTAACC
A D K V A K R L K V H G I L Q G Y G L T

1030 1040 1050 1060 1070 1080
GAPACCTGCAGCGCTCTAATACTTAGCCCCATGATCGAGAACTTAAAAAGGTGCAATT
E T C S A L I L S P N D R E L K K G A I

1090 1100 1110 1120 1130 1140
GGAACGCCTATGCCATATGTTCAAGTTAAAGTTATAGATATCAATACTGGGAAGGCGCTA
G T P M P Y V Q V K V I D I N T G K A L

1150 1160 1170 1180 1190 1200
GGACCAAGAGAAAAAGGCGAATATGCTTCAAAAGTCAATGCTTATGAAAGGATATCAC
G P R E K G E I C F K S Q M L M K G Y H

1210 1220 1230 1240 1250 1260
AACATCCGCAAGCAACTCGTGATGCTCTTGACAAAGATGGTTGGCTTCATACTGGGGAT
N N P Q A T R D A L D K D G W L H T G D

1270 1280 1290 1300 1310 1320
CTTGGATATTACGACGAAGACAGATTTATCTATGTAGTTGATCGATTGAAAGAACTTATT
L G Y Y D E D R F I Y V V D R L K E L I

1330 1340 1350 1360 1370 1380
AAATATAAAGGATATCAGGTTGCGCCTGCTGAACCTGGAAAACTGCTTTTACAACATCCA
K Y K G Y Q V A P A E L E N L L L Q H P

1390 1400 1410 1420 1430 1440
AATATTTCTGATGCGGGTGTATTGAATTCGGGACGAATTTGCTGGTCAATTACCTTTCC
N I S D A G V I E F R T N L L V N Y L S

1450 1460 1470 1480 1490 1500
GCGTGTGTTGTGTTAGAGCCTGGTAAGACAATGACCGAAAAGGAAGTTCAGGATTATATT
A C V V L E P G K T M T E K E V Q D Y I

FIG. 2B

1510 1520 1530 1540 1550 1560
GCAGAGCTAGTCACTACAACATAACATCTTCGAGGCGGTGTCGTATTTATAGATAGTATT
A E L V T T T K H L R G G V V F I D S I

1570 1580 1590 1600 1610 1620
CCAAAAGGCCCAACAGGAAAACTCATGAGAAACGAACTCCGAGCAATATTTGCCCCGGGAA
P K G P T G K L M R N E L R A I F A R E

1630 1640 1650 1660 1670 1680
CAGGCAAATCAAAATTATAAGCTCAATATATTGCTTTAGTTATAAAATGTATGTAATCA
Q A K S K L *

1690 1700 1710 1720
AATTTTAGAACCTAATACATTGAGAGCCTAAAAAAA

FIG. 2C

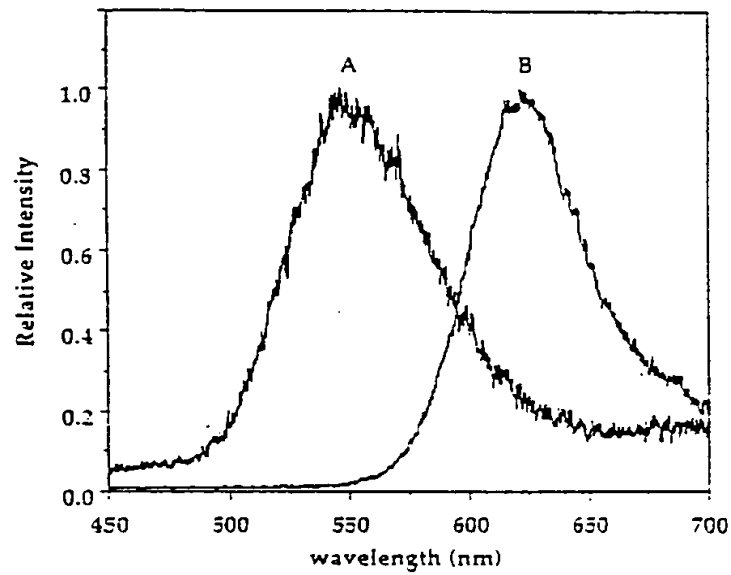


FIG. 3